

SCORE Search Results Details for Application 10070588 and Search Result us-10-070-588a-112.rge.

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OM nucleic - nucleic search, using sw model

Run on: April 20, 2006, 07:42:47 ; Search time 1831 Seconds
(without alignments)
341.495 Million cell updates/sec

Title: US-10-070-588A-112
Perfect score: 11
Sequence: 1 ctttggcacta 11

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_in:*
3: gb_env:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pr:*
9: gb_ro:*
10: gb_sts:*
11: gb_sy:*
12: gb_un:*
13: gb_vi:*
14: gb_htg:*
15: gb_pl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	% Query			DB	ID	Description
	No.	Score	Match Length			
c	1	11	100.0	11	6	AX099049 Sequence
	2	11	100.0	11	6	AX099050 Sequence
	3	11	100.0	18	6	AX201811 Sequence
	4	11	100.0	22	6	AX003312 Sequence
c	5	11	100.0	23	6	BD095189 Novel pol
c	6	11	100.0	47	6	AX427666 Sequence
	7	11	100.0	77	6	CQ057099 Sequence
	8	11	100.0	77	6	CQ076362 Sequence
	9	11	100.0	77	6	CQ107351 Sequence
	10	11	100.0	77	6	CQ146017 Sequence
	11	11	100.0	77	6	CQ205816 Sequence
	12	11	100.0	77	6	CQ229223 Sequence
	13	11	100.0	77	6	CQ267352 Sequence
	14	11	100.0	77	6	CQ304373 Sequence
	15	11	100.0	77	6	CQ341641 Sequence
	16	11	100.0	100	6	BD045829 Sequence
	17	11	100.0	100	6	AX910296 Sequence
	18	11	100.0	121	6	AX325267 Sequence
c	19	11	100.0	121	6	AX325268 Sequence
	20	11	100.0	129	10	G00343 sWSS785 Eri
	21	11	100.0	149	10	BX284306 Arabidops
c	22	11	100.0	150	6	CQ659646 Sequence
c	23	11	100.0	153	6	CQ058212 Sequence
c	24	11	100.0	153	6	CQ077548 Sequence
c	25	11	100.0	153	6	CQ108562 Sequence
c	26	11	100.0	153	6	CQ147196 Sequence
c	27	11	100.0	153	6	CQ182574 Sequence
c	28	11	100.0	153	6	CQ206983 Sequence
c	29	11	100.0	153	6	CQ230434 Sequence
c	30	11	100.0	153	6	CQ268567 Sequence
c	31	11	100.0	153	6	CQ305599 Sequence
c	32	11	100.0	153	6	CQ342787 Sequence
	33	11	100.0	167	10	AB152846 Homo sapi
	34	11	100.0	198	15	ATH553769 Arabidops
	35	11	100.0	201	10	BV201964 sqnm20783
c	36	11	100.0	204	5	AY847657 Darevskia
c	37	11	100.0	204	6	AX618370 Sequence
c	38	11	100.0	207	6	AR553184 Sequence
c	39	11	100.0	226	15	ATH526781 Arabidops
	40	11	100.0	232	10	BV084044 scl275_p3
	41	11	100.0	234	10	BX467061 Arabidops
	42	11	100.0	245	10	BX467053 Arabidops
c	43	11	100.0	246	6	CQ450823 Sequence
c	44	11	100.0	250	6	CQ920429 Sequence
	45	11	100.0	250	10	G15461 human STS S

ALIGNMENTS

RESULT 1
AX099049

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OM nucleic - nucleic search, using sw model

Run on: April 20, 2006, 07:34:22 ; Search time 287 Seconds
(without alignments)
255.441 Million cell updates/sec

Title: US-10-070-588A-112
Perfect score: 11
Sequence: 1 ctttggcacta 11

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_21:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*
14: geneseqn2005s:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	% Query Match	Length	DB	ID	Description
c	1	11	100.0	11	5	AAS02843	Aas02843 Human pre
	2	11	100.0	11	5	AAS02842	Aas02842 Human pre
c	3	11	100.0	17	8	ACD64825	Acd64825 HCV minus
	4	11	100.0	17	8	ACD57843	Acd57843 HCV DNazy
	5	11	100.0	17	8	ACD57844	Acd57844 HCV DNazy
c	6	11	100.0	17	8	ACD64826	Acd64826 HCV minus
	7	11	100.0	17	12	ADI83295	Adi83295 HCV DNazy
c	8	11	100.0	17	12	ADI86768	Adi86768 HCV DNazy
c	9	11	100.0	17	12	ADI86767	Adi86767 HCV DNazy
	10	11	100.0	17	12	ADI83296	Adi83296 HCV DNazy
	11	11	100.0	18	4	AAH23171	Aah23171 Nitric ox
	12	11	100.0	22	2	AAX85553	Aax85553 PCR prime
c	13	11	100.0	23	4	AAH24199	Aah24199 PCR prime
	14	11	100.0	33	5	AAH76792	Aah76792 Human bro
c	15	11	100.0	47	6	AAD38062	Aad38062 Maize pro
	16	11	100.0	77	4	AAI22229	Aai22229 Probe #12
	17	11	100.0	77	4	ABA67308	Aba67308 Human foe
	18	11	100.0	77	4	AAI47524	Aai47524 Probe #16
	19	11	100.0	77	4	ABA49398	Aba49398 Human bre
	20	11	100.0	77	4	AAK41482	Aak41482 Human bon
	21	11	100.0	77	4	AAK15744	Aak15744 Human bra
	22	11	100.0	77	4	ABS41072	Abs41072 Human liv
	23	11	100.0	77	5	AAI07928	Aai07928 Probe #79
	24	11	100.0	77	6	ABS15487	Abs15487 Human gen
	25	11	100.0	100	3	AAC22084	Aac22084 Human sec
c	26	11	100.0	121	6	ABK26046	Abk26046 Amino aci
	27	11	100.0	121	6	ABK26045	Abk26045 Amino aci
c	28	11	100.0	121	11	ADZ43021	Adz43021 Human gen
	29	11	100.0	121	12	ADN44736	Adn44736 Mutant ce
c	30	11	100.0	121	12	ADN44737	Adn44737 Mutant ce
	31	11	100.0	150	13	ADT77171	Adt77171 Type II d
c	32	11	100.0	153	4	AAI23415	Aai23415 Probe #13
c	33	11	100.0	153	4	ABA68523	Aba68523 Human foe
c	34	11	100.0	153	4	AAI48735	Aai48735 Probe #17
c	35	11	100.0	153	4	ABA50565	Aba50565 Human bre
c	36	11	100.0	153	4	ABA35504	Aba35504 Probe #13
c	37	11	100.0	153	4	AAK42661	Aak42661 Human bon
c	38	11	100.0	153	4	AAK16890	Aak16890 Human bra
c	39	11	100.0	153	4	ABS42283	Abs42283 Human liv
c	40	11	100.0	153	5	AAI09041	Aai09041 Probe #90
c	41	11	100.0	153	6	ABS16713	Abs16713 Human gen
c	42	11	100.0	204	8	ACF72987	Acf72987 Staphyloc
	43	11	100.0	213	6	ABS68966	Abs68966 Novel mur
c	44	11	100.0	240	6	ABL71901	Abl71901 Corn tass
	45	11	100.0	245	5	ABA11368	Aba11368 Human ner

ALIGNMENTS

RESULT 1
AAS02843/c
ID AAS02843 standard; DNA; 11 BP.

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OM nucleic - nucleic search, using sw model

Run on: April 20, 2006, 08:08:33 ; Search time 99 Seconds
(without alignments)
197.507 Million cell updates/sec

Title: US-10-070-588A-112
Perfect score: 11
Sequence: 1 ctttggcacta 11

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
1: /cgn2_6/ptodata/1/ina/1_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/H_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
7: /cgn2_6/ptodata/1/ina/PP_COMB.seq:*
8: /cgn2_6/ptodata/1/ina/RE_COMB.seq:*
9: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result %
Query

No.	Score	Match	Length	DB	ID	Description
1	11	100.0	25	3	US-09-396-196G-49096	Sequence 49096, A
2	11	100.0	25	3	US-09-396-196G-106030	Sequence 106030, A
3	11	100.0	25	3	US-09-396-196G-106031	Sequence 106031, A
4	11	100.0	100	3	US-09-513-999C-26159	Sequence 26159, A
c 5	11	100.0	207	3	US-09-248-796A-8315	Sequence 8315, Ap
6	11	100.0	276	3	US-09-513-999C-27111	Sequence 27111, A
c 7	11	100.0	305	3	US-09-270-767-26937	Sequence 26937, A
8	11	100.0	321	3	US-09-543-681A-963	Sequence 963, App
9	11	100.0	341	3	US-09-513-999C-3625	Sequence 3625, Ap
10	11	100.0	386	3	US-09-270-767-7666	Sequence 7666, Ap
11	11	100.0	386	3	US-09-270-767-22948	Sequence 22948, A
12	11	100.0	396	3	US-09-640-173-30	Sequence 30, Appl
13	11	100.0	396	3	US-09-713-550-30	Sequence 30, Appl
14	11	100.0	396	3	US-09-825-294-30	Sequence 30, Appl
15	11	100.0	396	3	US-09-970-966-30	Sequence 30, Appl
c 16	11	100.0	424	3	US-09-621-976-17465	Sequence 17465, A
c 17	11	100.0	475	3	US-09-621-976-2058	Sequence 2058, Ap
c 18	11	100.0	477	3	US-09-248-796A-2902	Sequence 2902, Ap
c 19	11	100.0	505	3	US-09-621-976-15675	Sequence 15675, A
c 20	11	100.0	551	3	US-09-647-224A-21	Sequence 21, Appl
21	11	100.0	552	3	US-09-134-000C-1129	Sequence 1129, Ap
c 22	11	100.0	570	3	US-09-517-790-3	Sequence 3, Appli
23	11	100.0	573	3	US-09-533-559-1998	Sequence 1998, Ap
c 24	11	100.0	579	3	US-09-640-211A-264	Sequence 264, App
25	11	100.0	601	3	US-09-949-016-20441	Sequence 20441, A
26	11	100.0	601	3	US-09-949-016-20442	Sequence 20442, A
c 27	11	100.0	601	3	US-09-949-016-23566	Sequence 23566, A
c 28	11	100.0	601	3	US-09-949-016-25590	Sequence 25590, A
c 29	11	100.0	601	3	US-09-949-016-29497	Sequence 29497, A
30	11	100.0	601	3	US-09-949-016-35684	Sequence 35684, A
31	11	100.0	601	3	US-09-949-016-35685	Sequence 35685, A
32	11	100.0	601	3	US-09-949-016-35718	Sequence 35718, A
33	11	100.0	601	3	US-09-949-016-35719	Sequence 35719, A
34	11	100.0	601	3	US-09-949-016-35752	Sequence 35752, A
35	11	100.0	601	3	US-09-949-016-35753	Sequence 35753, A
36	11	100.0	601	3	US-09-949-016-36869	Sequence 36869, A
c 37	11	100.0	601	3	US-09-949-016-45724	Sequence 45724, A
c 38	11	100.0	601	3	US-09-949-016-49633	Sequence 49633, A
c 39	11	100.0	601	3	US-09-949-016-49634	Sequence 49634, A
40	11	100.0	601	3	US-09-949-016-56559	Sequence 56559, A
c 41	11	100.0	601	3	US-09-949-016-60165	Sequence 60165, A
c 42	11	100.0	601	3	US-09-949-016-60166	Sequence 60166, A
43	11	100.0	601	3	US-09-949-016-66919	Sequence 66919, A
44	11	100.0	601	3	US-09-949-016-66920	Sequence 66920, A
45	11	100.0	601	3	US-09-949-016-67654	Sequence 67654, A

ALIGNMENTS

RESULT 1

US-09-396-196G-49096
 ; Sequence 49096, Application US/09396196G
 ; Patent No. 6821724
 ; GENERAL INFORMATION:
 ; APPLICANT: Michael Mittmann
 ; APPLICANT: David Mack
 ; APPLICANT: David Lockhart
 ; APPLICANT: Affymetrix, Inc.

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OM nucleic - nucleic search, using sw model

Run on: April 20, 2006, 08:23:25 ; Search time 433 Seconds
(without alignments)
210.077 Million cell updates/sec

Title: US-10-070-588A-112
Perfect score: 11
Sequence: 1 ctttggcacta 11

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA_Main:*
1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
3: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
4: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
5: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
6: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
7: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
8: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:*
9: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*
10: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

%

Result No.	Score	Query Match	Length	DB	ID	Description
1	11	100.0	17	3	US-09-740-332-541	Sequence 541, App
2	11	100.0	17	3	US-09-740-332-542	Sequence 542, App
c 3	11	100.0	17	3	US-09-740-332-4013	Sequence 4013, Ap
c 4	11	100.0	17	3	US-09-740-332-4014	Sequence 4014, Ap
5	11	100.0	17	3	US-09-817-879-541	Sequence 541, App
6	11	100.0	17	3	US-09-817-879-542	Sequence 542, App
c 7	11	100.0	17	3	US-09-817-879-4013	Sequence 4013, Ap
c 8	11	100.0	17	3	US-09-817-879-4014	Sequence 4014, Ap
9	11	100.0	17	7	US-10-669-841-3134	Sequence 3134, Ap
10	11	100.0	17	7	US-10-669-841-3135	Sequence 3135, Ap
c 11	11	100.0	17	7	US-10-669-841-6606	Sequence 6606, Ap
c 12	11	100.0	17	7	US-10-669-841-6607	Sequence 6607, Ap
13	11	100.0	18	3	US-09-769-207A-20	Sequence 20, Appl
14	11	100.0	18	6	US-10-268-311-20	Sequence 20, Appl
15	11	100.0	25	7	US-10-681-773-30008	Sequence 30008, A
16	11	100.0	25	7	US-10-681-773-42566	Sequence 42566, A
17	11	100.0	25	7	US-10-681-773-48158	Sequence 48158, A
18	11	100.0	25	7	US-10-681-773-96687	Sequence 96687, A
19	11	100.0	25	7	US-10-719-956-33153	Sequence 33153, A
c 20	11	100.0	25	7	US-10-719-956-193035	Sequence 193035,
c 21	11	100.0	25	7	US-10-719-956-193036	Sequence 193036,
22	11	100.0	25	7	US-10-719-956-311698	Sequence 311698,
23	11	100.0	25	7	US-10-719-956-596700	Sequence 596700,
24	11	100.0	25	8	US-10-719-900-240069	Sequence 240069,
25	11	100.0	25	8	US-10-719-900-250890	Sequence 250890,
26	11	100.0	25	8	US-10-719-900-299090	Sequence 299090,
c 27	11	100.0	25	8	US-10-719-900-326809	Sequence 326809,
c 28	11	100.0	25	8	US-10-719-900-350979	Sequence 350979,
29	11	100.0	25	8	US-10-719-900-380808	Sequence 380808,
c 30	11	100.0	25	8	US-10-719-900-513492	Sequence 513492,
c 31	11	100.0	25	8	US-10-719-900-513493	Sequence 513493,
c 32	11	100.0	25	8	US-10-719-900-640961	Sequence 640961,
c 33	11	100.0	25	8	US-10-719-900-686949	Sequence 686949,
34	11	100.0	25	8	US-10-719-900-692642	Sequence 692642,
c 35	11	100.0	25	8	US-10-719-900-801302	Sequence 801302,
36	11	100.0	25	8	US-10-719-900-929715	Sequence 929715,
37	11	100.0	25	8	US-10-719-900-976648	Sequence 976648,
38	11	100.0	25	8	US-10-719-900-977569	Sequence 977569,
39	11	100.0	25	9	US-10-809-189-49096	Sequence 49096, A
40	11	100.0	25	9	US-10-809-189-106030	Sequence 106030,
41	11	100.0	25	9	US-10-809-189-106031	Sequence 106031,
42	11	100.0	25	9	US-10-956-157-126297	Sequence 126297,
43	11	100.0	25	9	US-10-956-157-148462	Sequence 148462,
44	11	100.0	25	9	US-10-956-157-148524	Sequence 148524,
45	11	100.0	25	9	US-10-956-157-218919	Sequence 218919,

ALIGNMENTS

RESULT 1

US-09-740-332-541

; Sequence 541, Application US/09740332

; Publication No. US20030125270A1

; GENERAL INFORMATION:

; APPLICANT: Ribozyne Pharmaceuticals Inc.

; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Rela

; TITLE OF INVENTION: Hepatitis C Virus Infection

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OM nucleic - nucleic search, using sw model

Run on: April 20, 2006, 08:36:46 ; Search time 1385 Seconds
(without alignments)
32.139 Million cell updates/sec

Title: US-10-070-588A-112
Perfect score: 11
Sequence: 1 ctttggcacta 11

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 9288580 seqs, 2023302648 residues

Total number of hits satisfying chosen parameters: 18577160

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_NA_New:*

- 1: /SIDS5/ptodata/2/pubpna/US08_NEW_PUB.seq:*
- 2: /SIDS5/ptodata/2/pubpna/US06_NEW_PUB.seq:*
- 3: /SIDS5/ptodata/2/pubpna/US07_NEW_PUB.seq:*
- 4: /SIDS5/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
- 5: /SIDS5/ptodata/2/pubpna/US09_NEW_PUB.seq:*
- 6: /SIDS5/ptodata/2/pubpna/US09_NEW_PUB.seq1:*
- 7: /SIDS5/ptodata/2/pubpna/US10_NEW_PUB.seq:*
- 8: /SIDS5/ptodata/2/pubpna/US10_NEW_PUB.seq1:*
- 9: /SIDS5/ptodata/2/pubpna/US10_NEW_PUB.seq2:*
- 10: /SIDS5/ptodata/2/pubpna/US10_NEW_PUB.seq3:*
- 11: /SIDS5/ptodata/2/pubpna/US11_NEW_PUB.seq:*
- 12: /SIDS5/ptodata/2/pubpna/US11_NEW_PUB.seq2:*
- 13: /SIDS5/ptodata/2/pubpna/US11_NEW_PUB.seq3:*
- 14: /SIDS5/ptodata/2/pubpna/US11_NEW_PUB.seq4:*
- 15: /SIDS5/ptodata/2/pubpna/US60_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	% Query Match	Length	DB	ID	Description
	1	11	100.0	18	8	US-10-310-914A-755142	Sequence 755142,
c	2	11	100.0	19	8	US-10-310-914A-722741	Sequence 722741,
	3	11	100.0	19	12	US-11-101-244-813025	Sequence 813025,
	4	11	100.0	19	12	US-11-101-244-813049	Sequence 813049,
c	5	11	100.0	19	12	US-11-101-244-913637	Sequence 913637,
c	6	11	100.0	19	12	US-11-101-244-913737	Sequence 913737,
c	7	11	100.0	19	12	US-11-101-244-913843	Sequence 913843,
	8	11	100.0	19	12	US-11-101-244-917542	Sequence 917542,
c	9	11	100.0	19	12	US-11-101-244-962874	Sequence 962874,
c	10	11	100.0	19	12	US-11-101-244-962889	Sequence 962889,
c	11	11	100.0	19	12	US-11-101-244-962909	Sequence 962909,
c	12	11	100.0	19	12	US-11-101-244-962915	Sequence 962915,
c	13	11	100.0	19	12	US-11-101-244-1103586	Sequence 1103586,
	14	11	100.0	19	12	US-11-101-244-1182623	Sequence 1182623,
	15	11	100.0	19	12	US-11-101-244-1319264	Sequence 1319264,
	16	11	100.0	19	12	US-11-101-244-1319268	Sequence 1319268,
	17	11	100.0	19	12	US-11-101-244-1371859	Sequence 1371859,
c	18	11	100.0	19	12	US-11-101-244-1381443	Sequence 1381443,
c	19	11	100.0	19	12	US-11-101-244-1499929	Sequence 1499929,
c	20	11	100.0	19	12	US-11-101-244-1499948	Sequence 1499948,
	21	11	100.0	19	13	US-11-083-784-813025	Sequence 813025,
	22	11	100.0	19	13	US-11-083-784-813049	Sequence 813049,
c	23	11	100.0	19	13	US-11-083-784-913637	Sequence 913637,
c	24	11	100.0	19	13	US-11-083-784-913737	Sequence 913737,
c	25	11	100.0	19	13	US-11-083-784-913843	Sequence 913843,
	26	11	100.0	19	13	US-11-083-784-917542	Sequence 917542,
c	27	11	100.0	19	13	US-11-083-784-962874	Sequence 962874,
c	28	11	100.0	19	13	US-11-083-784-962889	Sequence 962889,
c	29	11	100.0	19	13	US-11-083-784-962909	Sequence 962909,
c	30	11	100.0	19	13	US-11-083-784-962915	Sequence 962915,
c	31	11	100.0	19	13	US-11-083-784-1103586	Sequence 1103586,
	32	11	100.0	19	13	US-11-083-784-1182623	Sequence 1182623,
	33	11	100.0	19	13	US-11-083-784-1319264	Sequence 1319264,
	34	11	100.0	19	13	US-11-083-784-1319268	Sequence 1319268,
	35	11	100.0	19	13	US-11-083-784-1371859	Sequence 1371859,
c	36	11	100.0	19	13	US-11-083-784-1381443	Sequence 1381443,
c	37	11	100.0	19	13	US-11-083-784-1499929	Sequence 1499929,
c	38	11	100.0	19	13	US-11-083-784-1499948	Sequence 1499948,
	39	11	100.0	22	8	US-10-310-914A-708742	Sequence 708742,
	40	11	100.0	22	8	US-10-310-914A-881397	Sequence 881397,
	41	11	100.0	22	8	US-10-310-914A-882336	Sequence 882336,
	42	11	100.0	24	8	US-10-310-914A-532229	Sequence 532229,
c	43	11	100.0	25	9	US-10-934-048A-89109	Sequence 89109, A
c	44	11	100.0	25	14	US-11-121-849-27983	Sequence 27983, A
c	45	11	100.0	25	14	US-11-121-849-131802	Sequence 131802,

ALIGNMENTS

RESULT 1
US-10-310-914A-755142

SCORE Search Results Details for Application 10070588 and Search Result us-10-070-588a 112.rnpm.

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OM nucleic - nucleic search, using sw model

Run on: April 20, 2006, 08:18:23 ; Search time 4165 Seconds
(without alignments)
146.028 Million cell updates/sec

Title: US-10-070-588A-112
Perfect score: 11
Sequence: 1 ctttggcacta 11

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 79147668 seqs, 27645789525 residues

Total number of hits satisfying chosen parameters: 158295336

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending Patents_NA_Main:*

- 1: /cgn2_6/ptodata/1/pna/PCTUSA_COMB.seq:*
- 2: /cgn2_6/ptodata/1/pna/PCTUSB_COMB.seq:*
- 3: /cgn2_6/ptodata/1/pna/PCTUSC_COMB.seq:*
- 4: /cgn2_6/ptodata/1/pna/US06_COMB.seq:*
- 5: /cgn2_6/ptodata/1/pna/US075_COMB.seq:*
- 6: /cgn2_6/ptodata/1/pna/US076_COMB.seq:*
- 7: /cgn2_6/ptodata/1/pna/US077_COMB.seq:*
- 8: /cgn2_6/ptodata/1/pna/US078_COMB.seq:*
- 9: /cgn2_6/ptodata/1/pna/US079_COMB.seq:*
- 10: /cgn2_6/ptodata/1/pna/US080_COMB.seq:*
- 11: /cgn2_6/ptodata/1/pna/US081_COMB.seq:*
- 12: /cgn2_6/ptodata/1/pna/US082_COMB.seq:*
- 13: /cgn2_6/ptodata/1/pna/US083_COMB.seq:*
- 14: /cgn2_6/ptodata/1/pna/US084_COMB.seq:*
- 15: /cgn2_6/ptodata/1/pna/US085_COMB.seq:*
- 16: /cgn2_6/ptodata/1/pna/US086_COMB.seq:*
- 17: /cgn2_6/ptodata/1/pna/US087_COMB.seq:*

18: /cgn2_6/ptodata/1/pna/US088_COMB.seq:*
19: /cgn2_6/ptodata/1/pna/US089_COMB.seq:*
20: /cgn2_6/ptodata/1/pna/US090_COMB.seq:*
21: /cgn2_6/ptodata/1/pna/US091_COMB.seq:*
22: /cgn2_6/ptodata/1/pna/US092_COMB.seq:*
23: /cgn2_6/ptodata/1/pna/US093_COMB.seq:*
24: /cgn2_6/ptodata/1/pna/US094_COMB.seq:*
25: /cgn2_6/ptodata/1/pna/US095A_COMB.seq:*
26: /cgn2_6/ptodata/1/pna/US095B_COMB.seq:*
27: /cgn2_6/ptodata/1/pna/US095C_COMB.seq:*
28: /cgn2_6/ptodata/1/pna/US096A_COMB.seq:*
29: /cgn2_6/ptodata/1/pna/US096B_COMB.seq:*
30: /cgn2_6/ptodata/1/pna/US096C_COMB.seq:*
31: /cgn2_6/ptodata/1/pna/US097A_COMB.seq:*
32: /cgn2_6/ptodata/1/pna/US097B_COMB.seq:*
33: /cgn2_6/ptodata/1/pna/US098A_COMB.seq:*
34: /cgn2_6/ptodata/1/pna/US098B_COMB.seq:*
35: /cgn2_6/ptodata/1/pna/US099A_COMB.seq:*
36: /cgn2_6/ptodata/1/pna/US099B_COMB.seq:*
37: /cgn2_6/ptodata/1/pna/US099C_COMB.seq:*
38: /cgn2_6/ptodata/1/pna/US099D_COMB.seq:*
39: /cgn2_6/ptodata/1/pna/US099E_COMB.seq:*
40: /cgn2_6/ptodata/1/pna/US100A_COMB.seq:*
41: /cgn2_6/ptodata/1/pna/US100B_COMB.seq:*
42: /cgn2_6/ptodata/1/pna/US101_COMB.seq:*
43: /cgn2_6/ptodata/1/pna/US102A_COMB.seq:*
44: /cgn2_6/ptodata/1/pna/US102B_COMB.seq:*
45: /cgn2_6/ptodata/1/pna/US103A_COMB.seq:*
46: /cgn2_6/ptodata/1/pna/US103B_COMB.seq:*
47: /cgn2_6/ptodata/1/pna/US103C_COMB.seq:*
48: /cgn2_6/ptodata/1/pna/US103D_COMB.seq:*
49: /cgn2_6/ptodata/1/pna/US103E_COMB.seq:*
50: /cgn2_6/ptodata/1/pna/US103F_COMB.seq:*
51: /cgn2_6/ptodata/1/pna/US104_COMB.seq:*
52: /cgn2_6/ptodata/1/pna/US105_COMB.seq:*
53: /cgn2_6/ptodata/1/pna/US106A_COMB.seq:*
54: /cgn2_6/ptodata/1/pna/US106B_COMB.seq:*
55: /cgn2_6/ptodata/1/pna/US107A_COMB.seq:*
56: /cgn2_6/ptodata/1/pna/US107B_COMB.seq:*
57: /cgn2_6/ptodata/1/pna/US107C_COMB.seq:*
58: /cgn2_6/ptodata/1/pna/US107D_COMB.seq:*
59: /cgn2_6/ptodata/1/pna/US107E_COMB.seq:*
60: /cgn2_6/ptodata/1/pna/US107F_COMB.seq:*
61: /cgn2_6/ptodata/1/pna/US107G_COMB.seq:*
62: /cgn2_6/ptodata/1/pna/US108_COMB.seq:*
63: /cgn2_6/ptodata/1/pna/US109A_COMB.seq:*
64: /cgn2_6/ptodata/1/pna/US109B_COMB.seq:*
65: /cgn2_6/ptodata/1/pna/US109C_COMB.seq:*
66: /cgn2_6/ptodata/1/pna/US110A_COMB.seq:*
67: /cgn2_6/ptodata/1/pna/US110B_COMB.seq:*
68: /cgn2_6/ptodata/1/pna/US110C_COMB.seq:*
69: /cgn2_6/ptodata/1/pna/US110D_COMB.seq:*
70: /cgn2_6/ptodata/1/pna/US111A_COMB.seq:*
71: /cgn2_6/ptodata/1/pna/US111B_COMB.seq:*
72: /cgn2_6/ptodata/1/pna/US112_COMB.seq:*
73: /cgn2_6/ptodata/1/pna/US117_COMB.seq:*
74: /cgn2_6/ptodata/1/pna/US600_COMB.seq:*
75: /cgn2_6/ptodata/1/pna/US601_COMB.seq:*
76: /cgn2_6/ptodata/1/pna/US602A_COMB.seq:*
77: /cgn2_6/ptodata/1/pna/US602B_COMB.seq:*
78: /cgn2_6/ptodata/1/pna/US603_COMB.seq:*

SCORE Search Results Details for Application 10070588 and Search Result us-10-070-588a-112.rnpn.

Score Home Page	Retrieve Application List	SCORE System Overview	SCORE FAQ	Comments / Suggestions
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This page gives you Search Results detail for the Application 10070588 and Search Result us-10-070-588a-112.rnpn.

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OM nucleic - nucleic search, using sw model

Run on: April 20, 2006, 08:22:29 ; Search time 1105 Seconds
(without alignments)
30.831 Million cell updates/sec

Title: US-10-070-588A-112
Perfect score: 11
Sequence: 1 ctttggcacta 11

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 6788836 seqs, 1548564257 residues

Total number of hits satisfying chosen parameters: 13577672

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending_Patents_NA New:*
1: /SIDS5/ptodata/2/pna/PCT_NEW_COMB.seq:*
2: /SIDS5/ptodata/2/pna/US06_NEW_COMB.seq:*
3: /SIDS5/ptodata/2/pna/US07_NEW_COMB.seq:*
4: /SIDS5/ptodata/2/pna/US08_NEW_COMB.seq:*
5: /SIDS5/ptodata/2/pna/US09_NEW_COMB.seq:*
6: /SIDS5/ptodata/2/pna/US10_NEW_COMB.seq:*
7: /SIDS5/ptodata/2/pna/US10_NEW_COMB.seq1:*
8: /SIDS5/ptodata/2/pna/US11_NEW_COMB.seq:*
9: /SIDS5/ptodata/2/pna/US11_NEW_COMB.seq1:*
10: /SIDS5/ptodata/2/pna/US11_NEW_COMB.seq2:*
11: /SIDS5/ptodata/2/pna/US11_NEW_COMB.seq3:*
12: /SIDS5/ptodata/2/pna/US60_NEW_COMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result			%		DB	ID	Description
	No.	Score	Match	Length			
	1	11	100.0	18	7	US-10-310-914B-755142	Sequence 755142,
c	2	11	100.0	19	7	US-10-310-914B-722741	Sequence 722741,
	3	11	100.0	19	9	US-11-313-452-813025	Sequence 813025,
	4	11	100.0	19	9	US-11-313-452-813049	Sequence 813049,
c	5	11	100.0	19	9	US-11-313-452-913637	Sequence 913637,
c	6	11	100.0	19	9	US-11-313-452-913737	Sequence 913737,
c	7	11	100.0	19	9	US-11-313-452-913843	Sequence 913843,
	8	11	100.0	19	9	US-11-313-452-917542	Sequence 917542,
c	9	11	100.0	19	9	US-11-313-452-962874	Sequence 962874,
c	10	11	100.0	19	9	US-11-313-452-962889	Sequence 962889,
c	11	11	100.0	19	9	US-11-313-452-962909	Sequence 962909,
c	12	11	100.0	19	9	US-11-313-452-962915	Sequence 962915,
c	13	11	100.0	19	9	US-11-313-452-1103586	Sequence 1103586,
	14	11	100.0	19	9	US-11-313-452-1182623	Sequence 1182623,
	15	11	100.0	19	9	US-11-313-452-1319264	Sequence 1319264,
	16	11	100.0	19	9	US-11-313-452-1319268	Sequence 1319268,
	17	11	100.0	19	9	US-11-313-452-1371859	Sequence 1371859,
c	18	11	100.0	19	9	US-11-313-452-1381443	Sequence 1381443,
c	19	11	100.0	19	9	US-11-313-452-1499929	Sequence 1499929,
c	20	11	100.0	19	9	US-11-313-452-1499948	Sequence 1499948,
	21	11	100.0	22	7	US-10-310-914B-708742	Sequence 708742,
	22	11	100.0	22	7	US-10-310-914B-881397	Sequence 881397,
	23	11	100.0	22	7	US-10-310-914B-882336	Sequence 882336,
	24	11	100.0	24	7	US-10-310-914B-532229	Sequence 532229,
c	25	11	100.0	25	11	US-11-348-413-214842	Sequence 214842,
c	26	11	100.0	25	11	US-11-348-413-214843	Sequence 214843,
c	27	11	100.0	25	11	US-11-348-413-214844	Sequence 214844,
c	28	11	100.0	25	11	US-11-348-413-214845	Sequence 214845,
c	29	11	100.0	25	11	US-11-348-413-594450	Sequence 594450,
c	30	11	100.0	25	11	US-11-348-413-594451	Sequence 594451,
c	31	11	100.0	25	11	US-11-348-413-594452	Sequence 594452,
c	32	11	100.0	25	11	US-11-348-413-594453	Sequence 594453,
c	33	11	100.0	25	11	US-11-348-413-594454	Sequence 594454,
c	34	11	100.0	25	11	US-11-348-413-594455	Sequence 594455,
c	35	11	100.0	25	11	US-11-348-413-826579	Sequence 826579,
c	36	11	100.0	25	11	US-11-348-413-1264817	Sequence 1264817,
c	37	11	100.0	25	11	US-11-348-413-1264818	Sequence 1264818,
c	38	11	100.0	25	11	US-11-348-413-1264819	Sequence 1264819,
	39	11	100.0	26	7	US-10-310-914B-755156	Sequence 755156,
c	40	11	100.0	30	1	PCT-US05-10912-295	Sequence 295, App
	41	11	100.0	57	10	US-11-130-645B-437218	Sequence 437218,
c	42	11	100.0	59	10	US-11-130-645B-250214	Sequence 250214,
c	43	11	100.0	63	10	US-11-130-645B-350115	Sequence 350115,
c	44	11	100.0	63	10	US-11-130-645B-554167	Sequence 554167,
c	45	11	100.0	63	10	US-11-130-645B-693759	Sequence 693759,

ALIGNMENTS

RESULT 1

US-10-310-914B-755142

; Sequence 755142, Application US/10310914B

; GENERAL INFORMATION:

; APPLICANT: Bentwich, Isaac

SCORE Search Results Details for Application 10070588 and Search Result us-10-070-588a-112.rst.

Score Home	Retrieve Application	SCORE System	SCORE	Comments /
Page	List	Overview	FAQ	Suggestions

This page gives you Search Results detail for the Application 10070588 and Search Result us-10-070-588a-112.rst.

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OM nucleic - nucleic search, using sw model

Run on: April 20, 2006, 07:47:47 ; Search time 2302 Seconds
(without alignments)
223.570 Million cell updates/sec

Title: US-10-070-588A-112
Perfect score: 11
Sequence: 1 ctttggcacta 11

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_est3:*
4: gb_htc:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_est7:*
9: gb_gss1:*
10: gb_gss2:*
11: gb_gss3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	11	100.0	43	9	AZ636663	AZ636663 1M0495D12
c 2	11	100.0	68	7	CO866272	CO866272 Mdftrt3046
3	11	100.0	72	8	T77835	T77835 ydl6c08.s1
4	11	100.0	87	10	CG668957	CG668957 OST465420
c 5	11	100.0	88	1	AI631958	AI631958 wa38b09.x
c 6	11	100.0	88	9	BZ662266	BZ662266 SALK_0257
7	11	100.0	91	2	BG409256	BG409256 gb88g12.y
8	11	100.0	106	2	BE165421	BE165421 QV1-HT047
c 9	11	100.0	107	6	CF776000	CF776000 jaa28e10.
c 10	11	100.0	113	9	AZ517183	AZ517183 RPCI-11-5
11	11	100.0	116	2	BI130927	BI130927 G112P81Y
12	11	100.0	120	1	AW551508	AW551508 L0079H06-
c 13	11	100.0	120	2	BF901301	BF901301 IL2-MT017
14	11	100.0	120	7	CK105615	CK105615 UA25DPA07
15	11	100.0	121	2	BF352764	BF352764 IL3-HT061
16	11	100.0	122	9	AZ759838	AZ759838 1M0552P23
c 17	11	100.0	126	8	CX541905	CX541905 s13dNF0BD
c 18	11	100.0	127	6	CA345114	CA345114 675650 NC
c 19	11	100.0	129	6	CB352552	CB352552 ZF001-P00
c 20	11	100.0	130	10	CG918048	CG918048 CH240_137
c 21	11	100.0	138	1	AA508728	AA508728 nh68d08.s
22	11	100.0	138	2	BF545856	BF545856 UI-R-BT0-
23	11	100.0	140	4	AK207727	AK207727 Mus muscu
c 24	11	100.0	140	9	BH055493	BH055493 RPCI-24-2
c 25	11	100.0	141	1	AI965679	AI965679 sc76h06.y
26	11	100.0	143	8	DR430870	DR430870 nax36a12.
c 27	11	100.0	146	1	AA717598	AA717598 vp94a07.r
c 28	11	100.0	147	9	CC516068	CC516068 CH240_361
29	11	100.0	149	3	BM113996	BM113996 EST561532
30	11	100.0	149	3	BM405670	BM405670 EST579997
c 31	11	100.0	150	8	R57383	R57383 F2971 Fetal
32	11	100.0	152	7	CV071926	CV071926 EST4087 Z
c 33	11	100.0	153	7	CO321951	CO321951 EK186851.
34	11	100.0	155	7	CO331019	CO331019 EK297249.
35	11	100.0	156	6	CD054495	CD054495 HO01E06r
c 36	11	100.0	156	9	BZ654414	BZ654414 OGAMR91TM
37	11	100.0	159	1	AV013351	AV013351 AV013351
c 38	11	100.0	162	3	BP671035	BP671035 BP671035
39	11	100.0	162	9	BH390901	BH390901 AG-ND-138
40	11	100.0	164	5	BW485387	BW485387 BW485387
41	11	100.0	168	9	BZ654404	BZ654404 OGAMR91TC
c 42	11	100.0	168	10	CL954906	CL954906 OsIRUA005
c 43	11	100.0	169	8	DN605021	DN605021 EST00232
c 44	11	100.0	174	3	BQ294074	BQ294074 1091026B0
45	11	100.0	175	3	BQ080480	BQ080480 san33g10.

ALIGNMENTS

RESULT 1

AZ636663

LOCUS AZ636663 43 bp DNA linear GSS 13-DEC-2000

DEFINITION 1M0495D12R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0495D12 R, genomic survey sequence.

ACCESSION AZ636663

EAST Search History

Ref #	Hits	Search Query	DBs	Default Operator	Plurals	Time Stamp
L2	2	wojnowski adj leszek	US-PGPUB; USPAT; DERWENT	OR	ON	2006/06/07 10:29
L3	0	hustert near elisabeth	US-PGPUB; USPAT; DERWENT	OR	ON	2006/06/07 10:27
L6	349	pxr	US-PGPUB; USPAT; DERWENT	OR	ON	2006/06/07 10:29
L7	125	l6 and mutation	US-PGPUB; USPAT; DERWENT	OR	ON	2006/06/07 10:29
L8	35	l7 and cyp3a	US-PGPUB; USPAT; DERWENT	OR	ON	2006/06/07 10:30

=> d his

(FILE 'HOME' ENTERED AT 10:33:01 ON 07 JUN 2006)

FILE 'CAPLUS, MEDLINE, BIOSIS' ENTERED AT 10:33:15 ON 07 JUN 2006

	E WOJNOWSKI LESZEK /AU
L1	98 S E3
	E HUSTERT ELISABETH /AU
L2	34 S E3
L3	108 S L1 OR L2
L4	6 S L3 AND PXR
L5	2 S L4 AND MUTATION?
L6	1 DUP REM L5 (1 DUPLICATE REMOVED)
L7	94 S PXR AND MUTATION?
L8	28 S L7 AND CYP3A
L9	13 DUP REM L8 (15 DUPLICATES REMOVED)
L10	8 S L9 AND PY<2003